Figure 1

Stability Study of SAHH
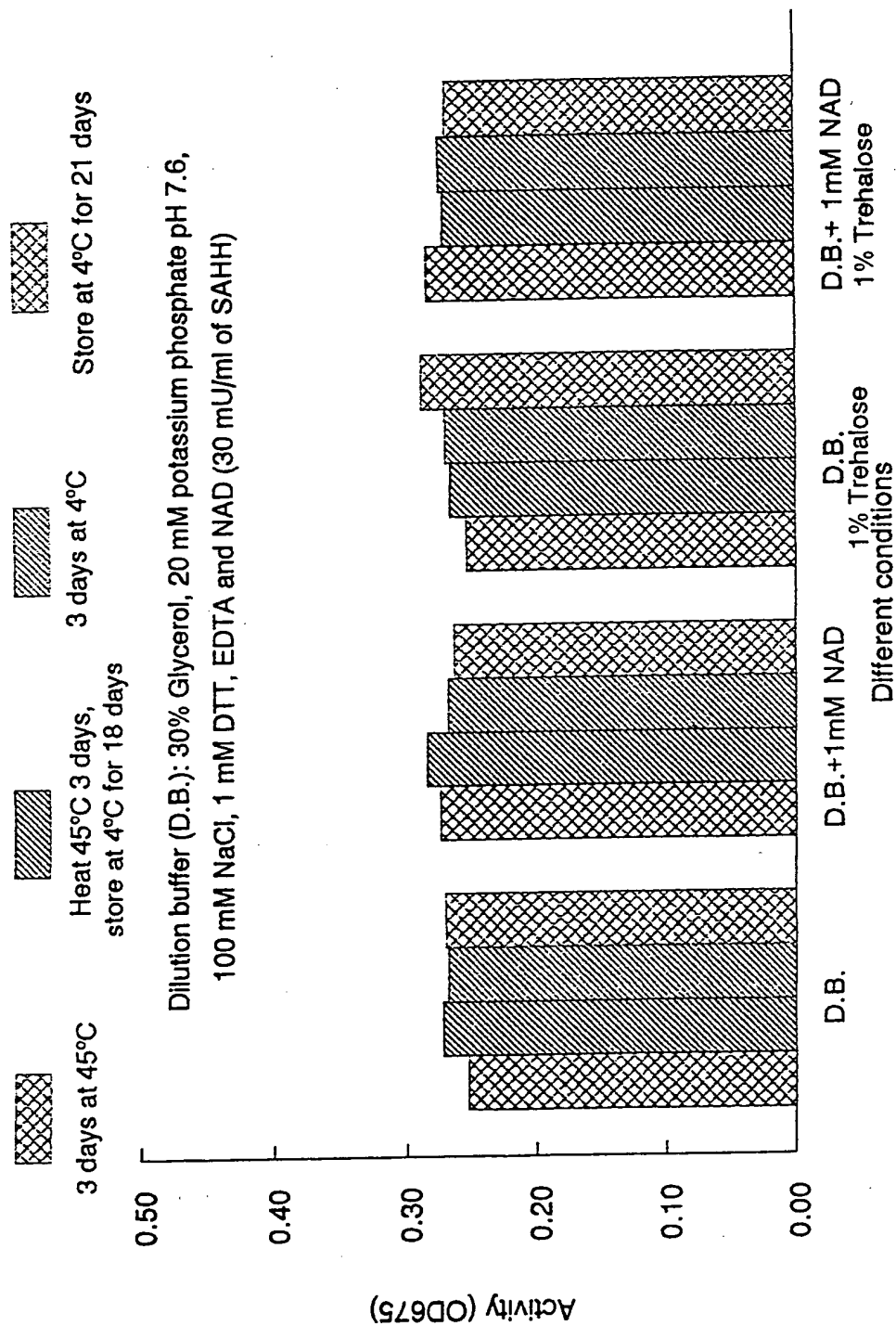

Legend:
- 3 days at 45°C
- Heat 45°C 3 days, store at 4°C for 18 days
- 3 days at 4°C
- Store at 4°C for 21 days

Dilution buffer (D.B.): 30% Glycerol, 20 mM potassium phosphate pH 7.6, 100 mM NaCl, 1 mM DTT, EDTA and NAD (30 mU/ml of SAHH)

X-axis (Different conditions): D.B., D.B.+1mM NAD, D.B. 1% Trehalose, D.B.+ 1mM NAD 1% Trehalose

Y-axis: Activity (OD675) — 0.00, 0.10, 0.20, 0.30, 0.40, 0.50

Figure 2

Screening of SAHH

Y-axis: OD675/OD600

X-axis values (top to bottom): 0.80, 0.60, 0.40, 0.20, 0.00

Bar labels:
- T7-7: 0.125
- Trc: 0.1
- Trc(9): 0.58

X-axis title: Diffrent Clones
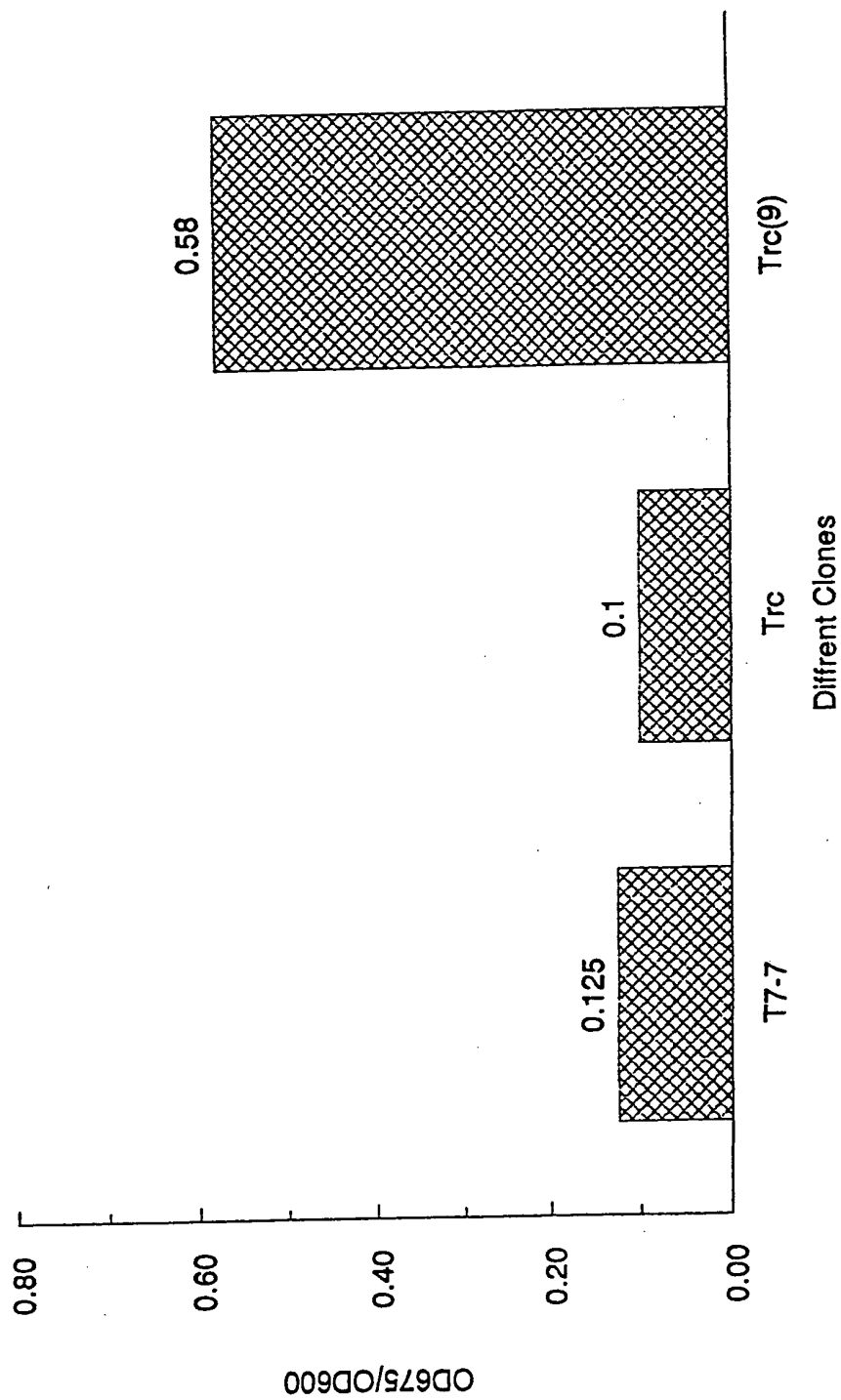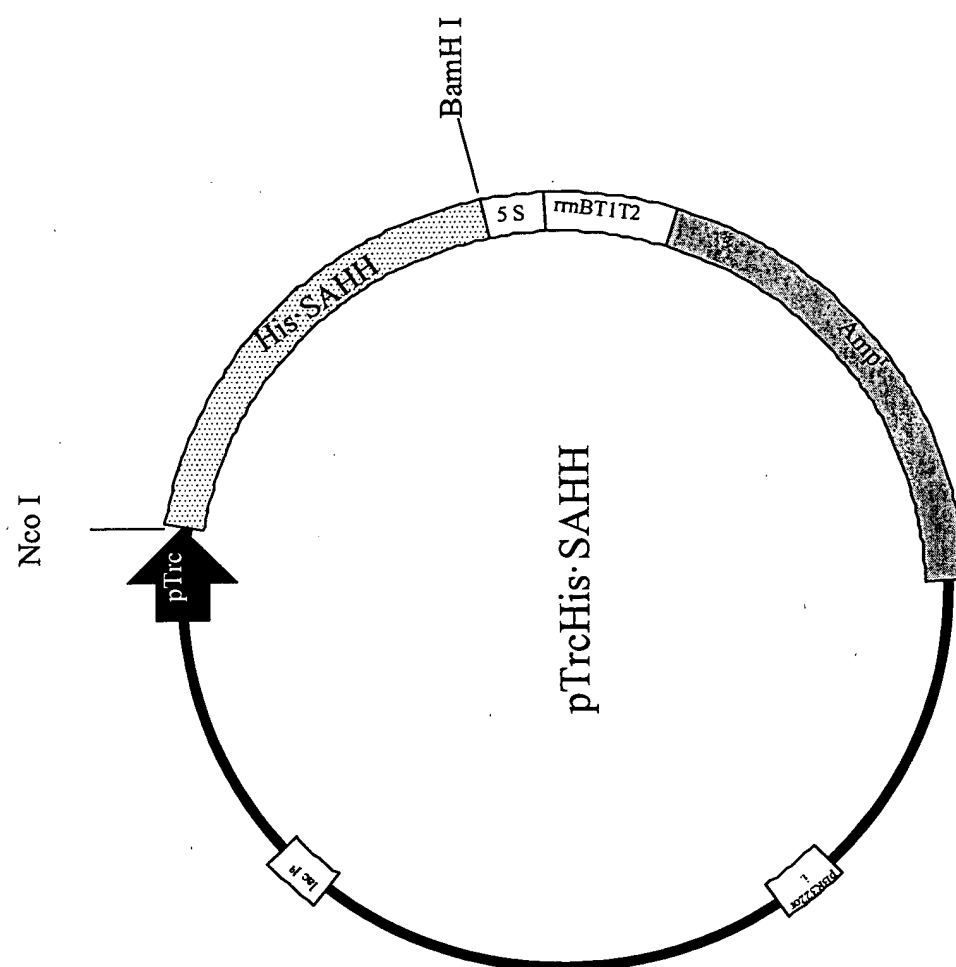
Figure 3

Figure 4

Stability of SAHH.His

3 days incubation in different temperature
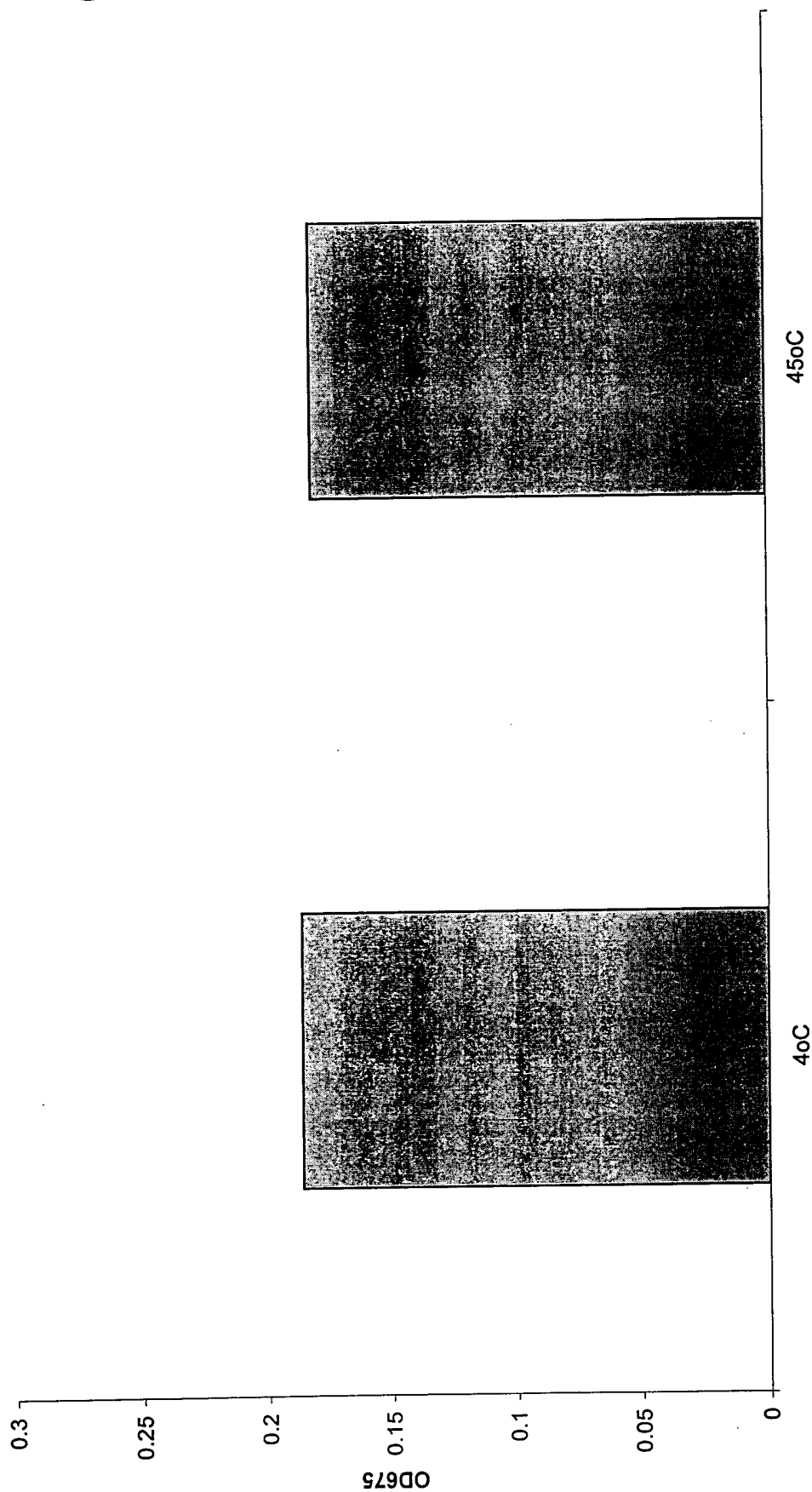
Figure 5
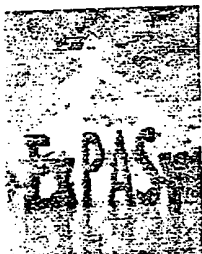
SIM - Results of the Alignment

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).
You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: Wild (1882 residues)
Sequence 2: A/C, (1594 residues)

using the parameters:

Number of alignments computed: 20
Cost of a matching aligned pair: 1
Cost of a transition: -1
Cost of a transversion: -1
Gap open penalty: 6.0
Gap extension penalty: 0.2

[Handwritten annotations:]
Accession
GenBank.   U 40872
TVU - 40872.   and
T vaginalis   ☐ g 111833 y
deposited
10/31/96
Bagnara, A S . F ...
Mol Biodun Parasit
(1996) 81 (-11

Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.
new

```
99.2% identity in 1461 residues overlap; Score: 1437.0; Gap frequency: 0.0%

Wild    291 ATGGCTTGCAAATCACCTGCTGGTGCTCCATTCGAGTACAGAATTGCCGACATCAACCTC
A/C,     71 ATGGCTTGCAAATCACCTACTGGTGCTCCATTCGAGTACAGAATTGCCGACATCAACCTC  SEQ ID NO.1
            ****************** *****************************************

Wild    351 CATGTTCTCGGCCGTAAGGAACTTACCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
A/C,    131 CATGTTCTCGGCCGTAAGGAACTTACCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
            ************************************************************

Wild    411 CTTCGTGAGCGTTATTCCGCTTCTAAGCCATTGAAGGGTGTCAGAATCTCTGGTTCCCTC
```

Figure 6a

```
A/C,       191 CTTCGT●●●GTTATTCCGCTTCTAAGCCATTGAAGGGTGTC●●ATCTCTGGTTCCCTC
               ******  ***************************************************

Wild       471 CACATGACAGTCCAGACAGCGGTCCTTATTGAGACACTCACAGCTCTTGGTGCTGATGTC
A/C,       251 CACATGACAGTCCAGACAGCCGTCCTCATCGAGACACTCACAGCTCTTGGTGCTGATGTC
               ******************** *****  ** *****************************

Wild       531 AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC
A/C,       311 AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC
               ***********************************************************

Wild       591 GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA
A/C,       371 GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA
               ***********************************************************

Wild       651 ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
A/C,       431 ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
               ***********************************************************

Wild       711 CCACAGCAGGTTGTCGATGATGGTGGTGATGCTACACTCCTCATCTCCAAGGGCTTCGAA
A/C,       491 CCACAGCAGGTTGTCGATGATGGTGGTGATGCTACACTCCTCATCTCCAAGGGCTTCGAA
               ***********************************************************

Wild       771 TTCGAAACAGCCGGTGCTGTCCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC
A/C,       551 TTCGAAACAGCCGGTGCTGTTCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC
               ******************** **************************************

Wild       831 GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCACTGGCACACAGTTGCT
A/C,       611 GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCACTGGCACACAGTTGCT
               ***********************************************************

Wild       891 GCCGGCATGAACGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACCAGCTC
A/C,       671 GCCGGCATGAACGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACCAGCTC
               ***********************************************************

Wild       951 GAGAAGGAGGGCAAACTCCTCTTCCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
A/C,       731 GAGAAGGAGGGCAAACTCCTCTTCCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
               ***********************************************************

Wild      1011 AAGTTCGATAACATCTACGGCTGTCGCCACTCCCTTATCGATGGTATCAACCGTGCTTCC
A/C,       791 AAGTTCGATAACATCTACGGCTGCCGCCACTCCCTTATCGATGGTATCAACCGTGCTTCC
               ***********************  **********************************

Wild      1071 GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTTACGGCGATGTCGGGAAGGGC
A/C,       851 GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTTACGGCGATGTCGGCAAGGGC
               ***************************************************** ******

Wild      1131 TGCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCTATC
A/C,       911 TGCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCAATC
               *******************************************************  ***

Wild      1191 TGCGCTCTCCAGGCTGTCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
A/C,       971 TGCGCTCTCCAGGCTGCCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
               ****************  *****************************************

Wild      1251 GATGTCGATATCTTCGTTACATGCACAGGAAACTGCGATATCATCTCTGTTGACATGATG
A/C,      1031 GATGTCGATATCTTCGTTACATGCACAGGAAACTGCGATATCATCTCTGTTGACATGATG
               ***********************************************************

Wild      1311 GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT
A/C,      1091 GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT
               ***********************************************************

Wild      1371 ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAATACGAC
```

Figure 6b

http://www.expasy.ch.cgi-out.sim.pr.net

```
A/C,       1151 ACAGAT●     ●CATGAAATACCCAGGCATCAAGCACATCCA●    ●AGCCAGAATACGAC
                ------**  ****************************************  *************

Wild       1431 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCCTTCTTAAC
A/C,       1211 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCCTTCTTAAC
                ******************************************************-****-

Wild       1491 CTTGGTTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTCACAAACCAGACA
A/C,       1271 CTTGGCTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTCACAAACCAGACA
                ***** ******************************************************

Wild       1551 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGATGAAGGTTTACACACTT
A/C,       1331 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGAAGAAGGTTTACACACTT
                *******************************************  ***************

Wild       1611 CCGAAGCATCTCGATGAAGAAGTCGTTCGCCTCCACCTCGGATCTCTCGATGTCCACCTT
A/C,       1391 CCGAAGCATCTCGATGAAGAAGTCGCTCGCCTCCACCTCGGATCTCTCGATGTCCACCTT
                ************************* **********************************

Wild       1671 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCCTTACAAG
A/C,       1451 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCCTTACAAG
                ************************************************************

Wild       1731 TCTGATGCTTACCGTTATTAA
A/C,       1511 TCTGATGCTTACCGTTATTAA
                *********************
```

65.9% identity in 44 residues overlap; Score: 14.0; Gap frequency: 0.0%

```
Wild        782 CGGTGCTGTCCCAGAGCCAACAGAAGCTGACAACCTCGAATACC
A/C,        682 CGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACC
                ***** *   *  **** ***** ** ** * *** *    ****
```

80.0% identity in 20 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild       1053 GGTATCAACCGTGCTTCCGA
A/C,        674 GGCATGAACGGTGTTTCCGA
                ** ** *** *** ******
```

87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild        564 GATACAGCCGCTGCTG
A/C,        554 GAAACAGCCGGTGCTG
                ** ******* *****
```

64.3% identity in 42 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild       1224 GTCCGCCGCATCGAGGAAGTCGTCAAGGATGTCGATATCTTC
A/C,        710 GTCCACCGCCTCTACCAGCTCGAGAAGGAGGGCAAACTCCTC
                **** **** ** *  *   *** ***** * *    ** **
```

87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild        774 GAAACAGCCGGTGCTG
A/C,        344 GATACAGCCGCTGCTG
                ** ******* *****
```

Figure 6c

12-27-1999 4:22 PM